

GenCore version 5.1.4-p5.4578
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 21:32:07 ; Search time 8449.13 Seconds

(without alignments)
117.112 Million cell updates/sec

Title: US-09-913-524-32

Perfect score: 34

Sequence: 1 aggcctccgaggaaccgagctgcccacatgcacact 34

Scoring table: IDENTIFY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank:*

1: gb_ba:*

2: gb_hg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pt:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vl:*

30: em_hlg_hum:*

31: em_hlg_inv:*

32: em_hlg_other:*

33: em_hlg_mus:*

34: em_hlg_pln:*

35: em_hlg_pod:*

36: em_hlg_man:*

37: em_hlg_vrl:*

38: em_sy:*

39: em_higo_hum:*

40: em_higo_mus:*

41: em_higo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	847	9	HS1NHAG2
2	34	100.0	1134	6	A14420
3	34	100.0	1237	6	A101843
4	34	100.0	1237	6	105264
5	34	100.0	1237	6	121913
6	34	100.0	1237	6	164619
7	34	100.0	1237	6	187901
8	34	100.0	1237	6	H0M1NHAA
9	34	100.0	1338	6	100529
10	34	100.0	1338	9	H0M1NHA
11	34	100.0	1393	9	BC006391
12	34	100.0	53239	2	AC011971
13	34	100.0	135033	9	AC009955
14	34	100.0	182662	2	AC024009
15	34	100.0	186883	2	AC040991
16	27.6	81.2	994	4	EC021219
17	27.6	81.2	1286	4	HRS1ASP
18	27.6	81.2	1372	10	AF432351
19	26	76.5	857	4	SRP1NHA
20	26	76.5	1144	10	RAT1NHBAB2
21	26	76.5	1160	10	MM1NAB
22	26	76.5	1182	4	BOV1NHA
23	26	76.5	1183	6	A14416
24	26	76.5	1183	10	MUS1NHB02
25	26	76.5	1328	10	MMALPHA
26	26	76.5	1561	10	RAT1NHA
27	26	76.5	101356	2	AC112361
28	24.4	71.8	731	4	AY028465
29	24.4	71.8	731	4	AY028466
30	24.4	71.8	1272	4	PIG1NHA
31	24.4	71.8	1333	4	SS1NHAR
32	24.4	71.8	1343	6	101835
33	24.4	71.8	1343	6	105231
34	24.4	71.8	1343	6	121910
35	24.4	71.8	1343	6	164616
36	24.4	71.8	1343	6	187898
37	22.6	66.5	180525	2	AC104750
38	21.8	64.1	11158	1	AE004682
39	21.8	64.1	113051	2	AC130781
40	21.8	64.1	240568	2	AC098942
41	21.4	62.9	84780	9	AC005885
42	21.4	62.9	150735	9	AC090687
43	21.4	62.9	193110	2	AC121839
44	21.4	62.9	237982	2	AC093483
45	21.2	62.4	140069	2	AC107245

ALIGNMENTS

RESULT 1

HS1NHAG2

LOCUS

DEFINITION H.sapiens inhA gene, exon 2.

ACCESSION X04446

VERSION X04446.1 GI:33924

KEYWORDS glycoprotein; glycoprotein hormone; hormone; inhibin; preprohormone.

SOURCE

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

Stewart,A.G., Milborrow,H.M., Ring,J.M., Crowther,C.E. and Forage,R.G.

TITLE Human inhibin genes. Genomic characterisation and sequencing
JOURNAL FEBS Lett. 206 (2), 329-334 (1986)
MEDLINE 87005283
PubMed 3758355

COMMENT See x04445 for exon 1.
Data kindly reviewed (05-JAN-1986) by Stewart A.

FEATURES Location/Qualifiers

source

1..847

/organism="Homo sapiens"

/db_xref="taxon:9606"

gene

5..847

exon

5..>847

misc_feature

172..174

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538..540

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Best Local Similarity 100.0%; Score 34; DB 9; Length 847;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCTCGGAGAACCGGCTGCCATGCCACT 34
Db 758 AGGCTCGGAGAACCGGCTGCCATGCCACT 791

RESULT 3

LOCUS 101843

DEFINITION Sequence 10 from Patent US 4798885.

ACCESSION 101843

VERSION 101843.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

Genentech, Inc.; South San Francisco, CA

Location/Qualifiers

1..1237

source

/organism="unknown"

BASE COUNT 210 a 431 c 346 g 250 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 34; DB 6; Length 1237;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCTCGGAGAACCGGCTGCCATGCCACT 34

Db 708 AGGCTCGGAGAACCGGCTGCCATGCCACT 741

RESULT 4

LOCUS 105264

DEFINITION Sequence 21 from Patent EP 0222491.

ACCESSION 105264

VERSION 105264.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

Patent: EP 0222491-A1 21-20-86; -1987;

Location/Qualifiers

1..1237

source

/organism="unknown"

BASE COUNT 210 a 431 c 346 g 250 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 34; DB 6; Length 1237;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCTCGGAGAACCGGCTGCCATGCCACT 34

Db 708 AGGCTCGGAGAACCGGCTGCCATGCCACT 741

RESULT 5

LOCUS 121913

DEFINITION Sequence 40 from patent US 5523488.

121913

1237 bp

DNA

Linear

PAT 07-OCT-1996

Query Match

Best Local Similarity 100.0%; Score 34; DB 6; Length 1134;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCTCGGAGAACCGGCTGCCATGCCACT 741

Db 708 AGGCTCGGAGAACCGGCTGCCATGCCACT 741

RESULT 5

LOCUS 121913

DEFINITION Sequence 40 from patent US 5523488.

121913

TITLE Human inhibin genes. Genomic characterisation and sequencing
JOURNAL FEBS Lett. 206 (2), 329-334 (1986)
MEDLINE 87005283
PubMed 3758355

COMMENT See x04445 for exon 1.
Data kindly reviewed (05-JAN-1986) by Stewart A.

FEATURES Location/Qualifiers

source

1..847

/organism="Homo sapiens"

/db_xref="taxon:9606"

gene

5..847

exon

5..>847

misc_feature

172..174

misc_feature

538..540

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ACCESSION 121913
 VERSION 121913.1 GI:1602267
 KEYWORDS
 SOURCE Unknown
 ORGANISM Unknown
 REFERENCE 1 (bases 1 to 1237)
 AUTHORS Mason,A.J. and Seeburg,P.H.
 TITLE Nucleic acid encoding the mature .alpha. chain of inhibin and method for synthesizing polypeptides using such nucleic acid
 JOURNAL Patent: US 5525488-A 40 11-JUN-1996;
 FEATURES
 source 1..1237
 /organism="unknown"
 BASE COUNT 210 a 431 c 346 g 250 t
 ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 0.017;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCTCCGAGAACCGCGCCATGCCCACT 34
 Db 708 AGGCTCCGAGAACCGCGCCATGCCCACT 741

RESULT 6
 LOCUS 164619 1237 bp DNA linear PAT 07-OCT-1997
 DEFINITION Sequence 40 from patent US 5665568.
 ACCESSION 164619
 VERSION 164619.1 GI:2481513
 KEYWORDS
 SOURCE Unknown
 ORGANISM Unknown
 REFERENCE 1 (bases 1 to 1237)
 AUTHORS Mason,A.J. and Seeburg,P.H.
 TITLE Nucleic acid encoding the mature .beta. sub-A chain of inhibin and method for synthesizing polypeptides using such nucleic acid
 JOURNAL Patent: US 5665568-A 40 09-SEP-1997;
 FEATURES
 source 1..1237
 /organism="unknown"
 BASE COUNT 210 a 431 c 346 g 250 t
 ORIGIN

Query Match 100.0%; Score 34; DB 6; Length 1237;
 Best Local Similarity 100.0%; Pred. No. 0.017;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCTCCGAGAACCGCGCCATGCCCACT 34
 Db 708 AGGCTCCGAGAACCGCGCCATGCCCACT 741

RESULT 7
 LOCUS 187901 1237 bp DNA linear PAT 10-AUG-1998
 DEFINITION Sequence 40 from patent US 5716810.
 ACCESSION 187901
 VERSION 187901.1 GI:3407841
 KEYWORDS
 SOURCE Unknown
 ORGANISM Unknown
 REFERENCE 1 (bases 1 to 1237)
 AUTHORS Mason,A.J. and Seeburg,P.H.
 TITLE Nucleic acid encoding the mature .beta. sub-B chain of inhibin and method for synthesizing polypeptides using such nucleic acid
 JOURNAL Patent: US 5716810-A 40 10-FEB-1998;
 FEATURES
 source 1..1237
 Location/Qualifiers

BASE COUNT 210 a 431 c 346 g 250 t
 ORIGIN

Query Match 100.0%; Score 34; DB 6; Length 1237;
 Best Local Similarity 100.0%; Pred. No. 0.017;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCTCCGAGAACCGCGCCATGCCCACT 34
 Db 708 AGGCTCCGAGAACCGCGCCATGCCCACT 741

RESULT 8
 LOCUS HUMINHAA 1247 bp mRNA linear PRI 06-JAN-1995
 DEFINITION Human ovarian alpha-inhibin mRNA.
 ACCESSION M13144
 VERSION M13144.1 GI:186412
 KEYWORDS
 SOURCE Human polycystic ovarian cDNA to mRNA, clones lambda-hin-alpha-12.61.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 1237)
 AUTHORS Mason,A.J., Niall,H.D. and Seeburg,P.H.
 TITLE Structure of two human ovarian inhibins
 JOURNAL Biochem. Biophys. Res. Commun. 135 (3), 957-964 (1986)
 MEDLINE 8618683
 PUBMED 3754442
 FEATURES
 source

Location/Qualifiers
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 /db_xref="taxon:9606"
 /map="2q33-qter"
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 /db_xref="GDB:300-120-100"
 /translation "GVSSGGLLEARELVIAVRAFLIDALGPATVRSQDPGARLR
 RRLALGQFTHRGSEPLEEDVSAQLLEFATTSSTEDKSARGLADEAEGLRFRFRP
 SQHRSKQVTSAGLWPHGTLDGCTAASNSSEPLIGLALSDGEPVAVPMISGAPPH
 MAVHLAISALSLTTHVAVLILRPVTSARIPETVAHRTTRPSSGGERARRS
 TRLMSWKSRSALDELQGGPEEAAHAKCHVAVLSDFILNMRMWLVYPSSEIHYC
 HGGGLHPNLSLQVPCAPVPAVYSLDIPGAPCCALPCTMRRLVHRTTSDGGYS
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 ORIGIN

BASE COUNT 210 a 431 c 346 g 250 t
 ORIGIN

Query Match 100.0%; Score 34; DB 9; Length 1237;
 Best Local Similarity 100.0%; Pred. No. 0.017;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCTCCGAGAACCGCGCCATGCCCACT 34
 Db 708 AGGCTCCGAGAACCGCGCCATGCCCACT 741

RESULT 9
 LOCUS 100529 1338 bp ss-DNA linear PAT 21-MAY-1993
 DEFINITION Sequence 1 from Patent US 4737578.
 ACCESSION 100529
 VERSION 100529.1 GI:768923
 KEYWORDS
 SOURCE Unknown
 ORGANISM Unknown

Query Match 100.0%; Score 34; DB 9; Length 1933;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCTCGGAGAACGGTGGCCATGCCAACT 34
 |||||||
 Db 840 AGGCTCGGAGAACGGCTGCCATGCCAACT 873

RESULT 12

AC011971

LOCUS

DEFINITION

AC011971

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUXILIOS

AC011971 53239 bp DNA linear HTG 13-JUL-2000
 Homo sapiens clone RP11-15J2, LOW-PASS SEQUENCE SAMPLING.

AC011971

AC011971.2 GI:7144910

HTG: HTGS_PHASE0.

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

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Homo sapiens

Submitted (17-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA.
 On Mar 3, 2000 this sequence version replaced g1:6065396.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIKR

Web site: http://www-seq.wi.mit.edu

Contact: sequence.submissions@genome.wi.mit.edu

Project Information

Center project name: L3480

Center clone name: 15_12

* NOTE: This record contains 59 individual
 * sequencing reads that have not been assembled into
 * contigs. Runs of N are used to separate the reads
 * and the order in which they appear is completely
 * arbitrary. Low-pass sequence sampling is useful for
 * identifying clones that may be gene-rich and allows
 * overlap relationships among clones to be deduced.
 * However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that
 * the record is updated, the accession number will
 * be preserved.

1 774: contig of 774 bp in length
 * 775 874: gap of 100 bp
 * 875 1662: contig of 788 bp in length
 * 1663 1762: gap of 100 bp
 * 1763 2553: contig of 791 bp in length
 * 2554 2653: gap of 100 bp

2654 3497: contig of 844 bp in length
 * 3498 3597: gap of 100 bp
 * 3598 4433: contig of 836 bp in length
 * 4434 4533: gap of 100 bp
 * 4534 5313: contig of 780 bp in length
 * 5314 5413: gap of 100 bp
 * 5414 6249: contig of 836 bp in length
 * 6250 6349: gap of 100 bp
 * 6350 7158: contig of 809 bp in length
 * 7159 7258: gap of 100 bp
 * 7259 8111: contig of 853 bp in length
 * 8112 8211: gap of 100 bp
 * 8212 9021: contig of 810 bp in length
 * 9022 9121: gap of 100 bp
 * 9122 9970: contig of 849 bp in length
 * 9971 10070: gap of 100 bp
 * 10071 10684: contig of 614 bp in length
 * 10685 10784: gap of 100 bp
 * 10785 11663: contig of 879 bp in length
 * 11664 11763: gap of 100 bp
 * 11764 12573: contig of 810 bp in length
 * 12574 12673: gap of 100 bp
 * 12674 13466: contig of 793 bp in length
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 * 14367 14466: gap of 100 bp
 * 14467 15278: contig of 812 bp in length
 * 15279 15378: gap of 100 bp
 * 15379 16186: contig of 808 bp in length
 * 16187 16286: gap of 100 bp
 * 16287 16977: contig of 691 bp in length
 * 16978 17077: gap of 100 bp
 * 17078 17860: contig of 783 bp in length
 * 17861 17960: gap of 100 bp
 * 17961 18841: contig of 881 bp in length
 * 18842 18941: gap of 100 bp
 * 18942 19724: contig of 783 bp in length
 * 19725 19824: gap of 100 bp
 * 19825 20560: contig of 736 bp in length
 * 20561 20660: gap of 100 bp
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 * 21455 22269: contig of 815 bp in length
 * 22270 22369: gap of 100 bp
 * 22370 23163: contig of 794 bp in length
 * 23164 23263: gap of 100 bp
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 * 29602 30332: contig of 731 bp in length
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 * 33027 33815: contig of 789 bp in length
 * 33816 33915: gap of 100 bp
 * 33916 34761: contig of 846 bp in length
 * 34762 34861: gap of 100 bp
 * 34862 35683: contig of 822 bp in length

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*	35784	36555:	contig of 772 bp	in length
*	36566	36655:	gap of	100 bp
*	36656	37524:	contig of 865 bp	in length
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*	37625	38433:	contig of 809 bp	in length
*	38434	38533:	gap of	100 bp
*	38534	39427:	contig of 894 bp	in length
*	39428	39527:	gap of	100 bp
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*	45843	45942:	gap of	100 bp
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*	46761	46860:	gap of	100 bp
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*	47698	47797:	gap of	100 bp
*	47798	48536:	contig of 799 bp	in length
*	48597	48696:	gap of	100 bp
*	48697	49501:	contig of 805 bp	in length
*	49502	49601:	gap of	100 bp
*	49602	50492:	contig of 881 bp	in length
*	50493	50592:	gap of	100 bp
*	50593	51425:	contig of 833 bp	in length
*	51426	51525:	gap of	100 bp
*	51526	52311:	contig of 786 bp	in length
*	52312	52411:	gap of	100 bp
*	52412	53239:	contig of 828 bp	in length

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/clone.lib="RPC1-11 Human Male BAC"
BASE COUNT      9751 a 10973 c 14398 g 10550 t 7567 others
ORIGIN

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Query Match	100.0%;	Score 34;	DB 2;	Length 53239;
Best Local Similarity	100.0%;	Pred. No. 0.013;		
Matches 34;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	AGGCTTCGGAGGAACCGGCTGCCCATGTCCAACT	34
Dd	AGGCCTCGGAGGAACCGGCTGCCCATGTCCAACT	119D

RESULT 13				
AC009955	AC009955	135033 bp	DNA	linear PRL 08-NOV-2000
LOCUS	Homo sapiens BAC clone RP11-256I23 from 2,	complete sequence.		
DEFINITION	AC009955			
ACCSSION	AC009955.4	GI:9581957		
VERSION	HTG.			
KEYWORDS				
SOURCE	Homo sapiens.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
REFERENCE	1 (bases 1 to 135033)			
AUTHORS	Sulston,J.F. and Waterston,R.			
TITLE	Toward a complete human genome sequence			
JOURNAL	Genome Res. 8 (11), 1097-1108 (1998)			
MEDLINE	99063792			
PUBMED	9847074			

REFERENCE	2 (bases 1 to 135033)
AUTHORS	Du,H., Maupin,R., Hawkins,M. and Hodges,J.
TITLE	The sequence of Homo sapiens BAC clone RP11-256123
JOURNAL	Unpublished
REFERENCE	3 (bases 1 to 135033)
AUTHORS	Waterston,R.H.
TITLE	Direct Submission
JOURNAL	Submitted (08-SEP-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE	4 (bases 1 to 135033)
AUTHORS	Waterston,R.H.
TITLE	Direct Submission
JOURNAL	Submitted (29-JUL-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE	5 (bases 1 to 135033)
AUTHORS	Waterston,R.H.
TITLE	Direct Submission
JOURNAL	Submitted (10-SEP-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE	6 (bases 1 to 135033)
AUTHORS	Waterston,R.
TITLE	Direct Submission
JOURNAL	Submitted (14-OCT-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE	7 (bases 1 to 135033)
AUTHORS	Waterston,R.
TITLE	Direct Submission
JOURNAL	Submitted (08-NOV-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT	On Jul29, 2000 this sequence version replaced gi:8569874.

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one clone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
The RPc1-11 human BAC library was made from the blood of one male donor, as described by Oseguwa, K., Moon, P. Y., Zhao, B., Frengen, E., Tateo, M., Calanese, J. J., and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)
VECTOR: pBAC3.6
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the right is RP11-51207, 200 base pair

Overlap. Actual start of this clone is at base position 1 of
RP11-256123; actual end is at base position 52326 of RP11-51207.

FEATURES

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Query Match 100.0%; Score 34; DR 9; Length 135033;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCTCGGAGAACGCGCCGCGCCGCGACCT 34
DB 46065 AGGCTCGGAGAACGCGCGCCGCGCCGCGACCT 46098

RESULT 14
AC024009 182662 bp DNA linear HTG 24-AUG-2002
LOCUS
DEFINITION Homo sapiens chromosome 2 clone RP11-158J14 map 2, WORKING DRAFT
ACCESSION
VERSION AC024009.2 GI:7210067
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 182662)
Birken,B., Linton,L., Nussbaum,C. and Lander,E.
Homo sapiens chromosome 2, clone RP11-158J14
JOURNAL
REFERENCE
2 (bases 1 to 182662)
Birken,B., Linton,L., Nussbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barina,N., Bede,F., Boguslavsky,L.,
Bouckhalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
Chospel,Y., Colangelo,M., Collins,S., Collumore,A., Cooke,P.,
Deatellano,K., Dewar,K., Dodge,S., Domino,M., Doyle,M.,
Penestor,J., Ferreira,P., Fitzhugh,M., Forrest,C., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,

Grand-Pierre, N., Grant, G., Hagos, B., Heatford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Laroque, K., Lehoczy, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Margulis, N., McCarthy, M., McEwan, P., McGuirk, A., McKernan, K., McSheeters, R., Meldrum, J., Menues, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Olivier, T.N., Peterson, K., Pierre, N., Pisanli, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Tirrell, A., Travers, M., Triggilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.-J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

TITLE
JOURNAL
REFERENCE
AUTHORS

Submitted (20-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 182662)

Direct Submission
 Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Mar 8, 2000 this sequence version replaced g17:008914.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RW/RepeatMasker.html

TITLE
JOURNAL
COMMENT

Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIRB
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu

Project Information
 Center project name: L7216
 Center clone name: 158.J.14

Summary Statistics
 Sequencing vector: M13; M77815; 100% of reads
 Chemistry: dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 162604 bases at least Q40
 Consensus quality: 171836 bases at least Q30
 Consensus quality: 176600 bases at least Q20
 Insert size: 180000; agarose-fp
 Insert size: 179762; sum-of-ctrls
 Quality coverage: 3.9 in Q20 bases; agarose-fp
 Quality coverage: 3.9 in Q20 bases; sum-of-ctrls

NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will

* be preserved.

1 37: contig of 37 bp in length
 38 137: gap of 100 bp
 138 1642: contig of 1505 bp in length
 1643 1742: gap of 100 bp
 1743 3192: contig of 1450 bp in length
 3193 3292: gap of 100 bp
 3293 4982: contig of 1690 bp in length
 4983 5082: gap of 100 bp
 5083 5645: contig of 563 bp in length
 5646 5745: gap of 100 bp
 5746 7669: contig of 1924 bp in length
 7670 7769: gap of 100 bp
 7770 9530: contig of 1761 bp in length
 9531 9630: gap of 100 bp
 9631 11783: contig of 2153 bp in length
 11784 11883: gap of 100 bp
 11884 14433: contig of 2550 bp in length
 14434 14533: gap of 100 bp
 14534 18392: contig of 3859 bp in length
 18393 18492: gap of 100 bp
 18493 23382: contig of 4890 bp in length
 23383 23482: gap of 100 bp
 23483 27364: contig of 3882 bp in length
 27365 27464: gap of 100 bp
 27465 32120: contig of 4656 bp in length
 32121 32220: gap of 100 bp
 32221 36450: contig of 4230 bp in length
 36451 36550: gap of 100 bp
 36551 41108: contig of 4558 bp in length
 41109 41208: gap of 100 bp
 41209 45527: contig of 4319 bp in length
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 50263 50362: gap of 100 bp
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 55363 55462: gap of 100 bp
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 61029 66694: contig of 5666 bp in length
 66695 66794: gap of 100 bp
 66795 73126: contig of 6532 bp in length
 73127 73226: gap of 100 bp
 73227 79690: contig of 6464 bp in length
 79691 79790: gap of 100 bp
 79791 87490: contig of 7700 bp in length
 87491 87590: gap of 100 bp
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 107345 107444: gap of 100 bp
 107445 117711: contig of 10277 bp in length
 117712 117811: gap of 100 bp
 117812 128059: contig of 10248 bp in length
 128060 128159: gap of 100 bp
 128160 143948: contig of 15789 bp in length
 143949 144048: gap of 100 bp
 144049 157783: contig of 13735 bp in length
 157784 157883: gap of 100 bp
 157884 182662: contig of 24779 bp in length.

FEATURES
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Best local similarity 100.0%; Pred. No. 0.012;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 AGGCTCCGAGAACCGCTGCCATGCCCAACT 34
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RESULT 15
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DEFINITION
ACCESSION      AC040991.2 GI:8014664
VERSION      HTG: HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE      1 (bases 1 to 186883)
AUTHORS      Birren,B., Linton,L., Nusbaum,C., Lander,E., Abramam,H., Allen,N.,
Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
Collamore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,
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Galagan,J., Gardyna,S., Glade,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heatford,A., Horton,L.,
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Levine,R., Lieu,C., Liu,G., Locke,K., MacDonald,P., Marquis,N.,
McCarthy,M., McKean,P., Mcurr,A., McKernan,K., Mcpheeters,R.,
Meitrim,D., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,

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TITLE
JOURNAL
REFERENCE
AUTHORS
Submitted (11-APR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 186883)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
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Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission

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TITLE
JOURNAL
COMMENT
Submitted (12-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 22, 2000 this sequence version replaced g1:7534193.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: 124_E_11
Center clone name: 124_E_11
----- Summary Statistics
Sequencing vector: R33 M77815; 100% of reads
Chemistry: Dye-termination Big Dye3; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 175185 bases at least Q40
Consensus quality: 181490 bases at least Q30
Consensus quality: 183848 bases at least Q20
Insert size: 190000; agarose-fp
Insert size: 185283; sum-of-coverage
Quality coverage: 4.3 in Q20 bases; agarose-fp
Quality coverage: 4.4 in Q20 bases; sum-of-coverage

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* NOTE: This is a 'working draft' sequence. It currently
* consists of 17 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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* 17481 22233: contig of 4753 bp in length
* 22234 22333: gap of 100 bp
* 22334 25600: contig of 3267 bp in length
* 25601 25700: gap of 100 bp
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* 31827 31926: gap of 100 bp
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* 41357 41456: gap of 100 bp
* 41457 53195: contig of 11739 bp in length
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* 53296 64559: contig of 11264 bp in length
* 64560 64659: gap of 100 bp
* 64660 79824: contig of 15165 bp in length
* 79825 79924: gap of 100 bp
* 79925 99909: contig of 19985 bp in length
* 99910 100009: gap of 100 bp
* 100010 121977: contig of 21968 bp in length
* 121978 122077: gap of 100 bp
* 122078 143182: contig of 21105 bp in length
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164688. .186883
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BASE COUNT 42272 a 51993 c 50631 g 40377 t 1610 others
ORIGIN
Query Match 100.0%; Score 34; DB 2; Length 186883;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGGCTCGGAGAGACGGCTCGCCATGTCACACT 34
|||||
DB 105583 AGGCTCGGAGAGACGGCTCGCCATGTCACACT 105550

Search completed: March 11, 2003, 09:14:22
Job time : 8545.13 secs

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4587. .9251
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/note="assembly_fragment"
100010. .121977
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122078. .143182
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164688. .186883
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